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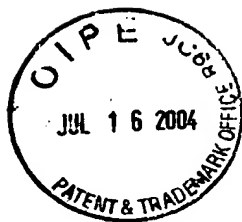
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48 KD G1 i-antigen : protein and nucleic acid sequences

[illegible]

Fig. 1

REPLACEMENT SHEET

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SEQ ID NO: 44 G5 Wild-type

10 20 30 40 50 60 70 80 90 100 110 120
ATCAAAAATA ATATTTTACT AATATTCATT ATTTTCATTAT TTATCAATTA AATTAAATCT GCTAATTTCTC CTCTTGGAAC TGAACCTAAC ACACCGCGAT AAGTTTGATGA TCTAGGAAC

130 140 150 160 170 180 190 200 210 220 230 240
CCCTGCAATTT GTGTAAATTC TTAGAAAAC TTTTATTATA ATAAATCTGC TGCTTTGGTT CCTTGGTCTA GTAGGTGTAC ACCTTGTCCA TAAAAAAAAG ATGCTGTGTGC TTAACCAAAAT

250 260 270 280 290 300 310 320 330 340 350 360
CCACCTGTCTA CTGCTAATTT AGTCACATAA TCTAAGGTTA AATGCCCTGC TGGTACCGCA ATTGCAGGTG GAGCAACAGA TTATGCCAGCA ATATCATCAG AATGTGTATA TTGTAGAAATT

370 380 390 400 410 420 430 440 450 460 470 480
AATTTTATA ATGAAATGC TCCAAATTTT AATGCAGGTG CTATAGTACG CACAGCTTGT CCGGTAAACA GAGTTGGTGG TGCATTTGACT GCTGTAAATG CCGCTACCANT AGTGGCATTA

490 500 510 520 530 540 550 560 570 580 590 600
TGTAACTGCG CATGTCTTAC TGGTACTGCA CTGTGATGATG GAGTAACTAC TGAATTATGT AGATCAITCA CAGAAATGTGT TAAATGTAGA CTTAACCTTTT ACTATAATGG TAATAATGCT

610 620 630 640 650 660 670 680 690 700 710 720
AATPACTGCTT TCAATCCAGG TAAAGTTAA TCCACACCTT TCCACACCTT TAAACCTGCT AATGTGCTT AAGCTACTTT AGGTAAATGAT GCTAACATAA CCGCATTAATG TAACGTTTGA

730 740 750 760 770 780 790 800 810 820 830 840
TGGCTGTATG GTACTATATG TGCCTGTGGA GTAAATTAAT GGSTAGCACA AAACACTGAA TGTACTTAAT GTGCTCTTAA CTTTTACAAT AATAATGCTC CTAAATTTTCAA TCCAGGTAAAT

850 860 870 880 890 900 910 920 930 940 950 960
AGTACATGCC TACCTTGGCC AGCAATAAA GATTATGCTG CTGAAGCCAC TGCAGGTGGT GCGGCTACTT TAGCCCAATA ATGTAAATAT GCATGCCCTG ATGGTACTGC AATTGCTACT

970 980 990 1000 1010 1020 1030 1040 1050 1060 1070 1080
GGAGCACTA ATTATGTAAT ATTATAAACA GAATGTCTAA ATTGTGCTGC TAACCTTTAT TTGTATGCTA ATAAATTTCTA GGCAGGAAGT AGTAGATGCA AAGCATGTGC AGCAATAAA

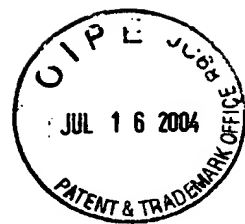
1090 1100 1110 1120 1130 1140 1150 1160 1170 1180 1190 1200
GTTTAAAGCG CTGTASCAAC TGCAGGTGGT ACTGTACTTT TAATTGCTAT ATGTGCCCTT GAATGCCCTG CTGGTACTGT ACTCACCGAT GGAACAACAT CTACTTATAA ATTAAGCGCA

1210 1220 1230 1240 1250 1260 1270 1280 1290 1300 1310 1320
TCTGAATGCG TTAAATGTGC TGCCAACTTT TATACTACAA AATAAACTGA TTGGSTAGCA GGTATGATA CATGTACTAG TTGTAAATAA AAATTAACCT CTGGCGCTGA AGCTAAATTTA

1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430 1440
CCGTAACTCG CTAAAAAAA TATATAATGT GAATTTGGCTA AATTTTATC AATTTCCTTA TTATTTGATTT CTATTAATTT ATTAATGATGA 1440

Coding region: nucleotides 1-1404

Fig. 2a



REPLACEMENT SHEET

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G5 SYNTHETIC

10	20	30	40	50	60	70	80	90	100	110	120
ATGAAGAACA	ACATCTCTGT	GATCCTGTAT	ATCTCTCTGT	TCATCAACCA	GATCAAGTCT	GCTAACTGTC	CTGTGGGAAC	CGAGACCAAC	ACCCTGGAC	AGGTGGACGA	CCTGGGAACC
130	140	150	160	170	180	190	200	210	220	230	240
CCTGCTAACT	GTGTGAACCT	TCAGAAGAAC	TTCTACTACA	ACAACGCTGC	TGCTTTGGTG	CCTGGAGCTT	CTAACCTGTAC	CCCTTGTCTT	CAGAAGAAGG	ACGCTGGAGC	TCAGCCTAAC
250	260	270	280	290	300	310	320	330	340	350	360
CCTCTCTGTA	CCGCTAACTT	GGTGAACCCAG	TGTAAAGTGA	AGTGTCTCTG	TGGAACCGCT	ATCCTCTGAG	GAGCTAACGA	CTAACGCTGT	ATCATCAACG	AGTGTGTGAA	CTGTGCGATC
370	380	390	400	410	420	430	440	450	460	470	480
AACCTCTACA	ACGAGAACGC	TCTTAACCTT	AACGCTGGAG	CTTCTAACCTG	TACCGCTTGT	CCTGTGAACC	GGCTGGGAGG	AGCTCTGACC	GCTGGAAACG	CTGTACACAT	CGTGGCTCAG
490	500	510	520	530	540	550	560	570	580	590	600
TGTAAAGTGG	CTTGTCTTAC	CGGAACCGCT	CTGGAGGACG	GAGTGACAC	CGACTACGTC	CGCTCTTTTCA	CCGAGTGTGT	GAGGTGTGCG	CTGAACCTTCT	ACTACAAACGG	AAACAACGGA
610	620	630	640	650	660	670	680	690	700	710	720
AACACCCCTT	TCAAACCTGG	AAAGTCTCAG	TGTAAACCTT	GTCTGTCTAT	CAAGCTGCT	AACGTGGCTC	AGGCTAACCTT	GGGAAACGAC	GCTTACCATCA	CCGCTCAGTG	TAACTGTGCT
730	740	750	760	770	780	790	800	810	820	830	840
TGTCTGACG	GAACCATCTC	TGCTCTCTGA	GTGAACCACT	GGGTGGCTCA	GAACACCGAG	TGTAAACCACT	GTGCTCTTAA	CTTCTTACAC	AACAACGCTC	CTAACCTTCA	CCCTGGAAAC
850	860	870	880	890	900	910	920	930	940	950	960
TCTAACCTGC	TGCTTGTGTC	TGCTTAACAG	GACTAAGGAG	CTGAGGCTAC	CGCTGGAGGA	GCTCTTACCC	TGGCTTAAGCA	GTGTAAACATC	GCTTGTCTTG	ACGGAAACGC	TATGTGCTCT
970	980	990	1000	1010	1020	1030	1040	1050	1060	1070	1080
GGAGCTTACA	ACTTACCTGAT	CCTGAGAAC	GAGTGTCTGA	ACTGTGCTGC	TAACTTCTTAC	TTGAGAGGAA	ACAACTTCCA	GGCTGGATCT	TCTGGCTGTA	AGGCTTGTCC	TGCTTAACAG
1090	1100	1110	1120	1130	1140	1150	1160	1170	1180	1190	1200
GTGAGGGGAG	CTGTGGCTTAC	CGCTGGAGGA	ACCCTTACCC	TGATCGCTCA	GTGTGCTCTG	GAGTGTCTCTG	CTGGAAACCGT	GCTGAACCGAC	GGAAACCACT	CTAACCTTAA	CGAGGCTGCT
1210	1220	1230	1240	1250	1260	1270	1280	1290	1300	1310	1320
TCTGAGTGTG	TGAAAGTGTG	TGCTTAACCTT	TACACACCCA	AGCAGACCGA	CTGGGTGGCT	GGATGTGACA	CCTGTACCTC	TTGTAAACAG	AAGCTGACTT	CTGGAGCTGA	GGCTTAACCTG
1330	1340	1350	1360	1370	1380	1390	1400	1410	1420	1430	1440
CCTGAGTCTG	CTAAGAGAGAA	CATCCAGTGT	GACTTGTGCTA	ACTTCTGCTC	TATCTCTCTG	CTGCTGATCT	CTTACTACTCT	GCTGTATTA

Coding region: nucleotides 1-1404

Fig. 2b

REPLACEMENT SHEET

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Sequence Alignment of 48 kD G1 i-antigen
and 55 kD G5 i-antigen protein sequences

SEQ ID NO: 6	G1	Conserved regions
SEQ ID NO: 7	G5	
1	1	MKYNILLILISLFINELRAVPCPDGTQT-QAG-LTDVGAADLGTCTVNCRPNFYNN----
	1	MKNILVILLISLFINQIKSANCVPVGTETNTAGQVDDLTGP--ANCVCQKPNFYNNAAA
		** ***:***** ** ** * * * * * ; * * * * * *****
55	55	--GGAA-----QGEANGNP-----
59	59	FVPGASTCTPCPKKDKAGAPPPATANLVTCQNVKCPAGTAAGGATDYAAIITECVNC
		** * * * * ; * * *
68	68	---F-----AAN-NAARGICVPCQINRVGSVTNAGDLATLATQCTCPTGTALDDGVTIDV
119	119	RINFYNENAPNPNAGASTCTACPVNRVGGALTAGNAATIVACNVACPTGTALDDGVTID
		* * * * * ; * * * * * *****
120	120	FDRSAAQCVKCKPNFYNGSPQGEAPGVQVFAAGAAAAGVAAVTSQCVCPLNK--NDS
179	179	YVRSFTECVKCRNLNFYNGNN--GNTP-----FNPGK-----SQCTPCPAIKPANVA
		: * * * * * : * * * * * * * * * * * * * * *
178	178	PATAGAQANLATQCSNQCPTGTVLDDGVTLVFNTSATLCVKCRPNFYNGSPQGEAPGV
224	224	QATLGNDAITATQCNVACPDGTISAAGVN-NWVAQNTCTNCAPNFYNN-----AP--
		** * * * * : * * * * * * * * * * * * * * *
238	238	QVFAAGAAAAGVAAVTSQCVCQINKNND-SPATAGAQANLATQCTCPTGTAIQDGVTL
295	295	-NFNPG-----NSTCLPCPANKDYGAEATAGGAATLAKQCNACPDGTAIASGATN
		* * * * * * * * * * : * * * * * * * * * * . . .
297	297	VFSNSTQCSQCIANYFENG-NFEAGKSQCLKCPVSKTTPAHAP-GNTATQATQCLTICP
325	325	-YVILQTECLNCAANFYFDGNNFQAGSSRCACPANKVQGVATAGGTATLIAQCALECP
		: * * * * * : * * * * * : * * * * * : * * * * * * * * * *
355	355	AGTVLDDGTSNFWASATECTKCSAGFFASKTGTGTAGTDTCTECKKLTSGATAKVAE
384	384	AGTVLTDGTTSTYKQAASECVKCAANFYTTKQTDWVAGIDTCTSCNKKLTSGAEANLPES
		***** * * * * : * * * * * * * * * * * * * * *
415	415	ATQKVQCASTTFAKFLSISLLFISFYLL
444	444	AKKNIQCD---FANFLSISLLLSFYLL
		* * * * * : * * * * * * * * * * * * * * *
		Conserved regions MKYNILLILISLFIN MKNILVILLISLFIN
90	90	
91	91	
92	92	CPTGTALDDGVT
93	93	CVKCKPNFYNG
94	94	CVKCRNLNFYNG
95	95	CPAGTVLDDGT
96	96	CPAGTVLTDGT
97	97	AGTDTCTECKKLTSGATA
98	98	AGIDTCTSCNKKLTSGAEA
99	99	FAKFLSISLLFISFYLL
100	100	FANFLSISLLLSFYLL

Fig. 3a

REPLACEMENT SHEET

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Fig. 3b₁

Fig. 3b₂

Fig. 3b



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Fig. 3b₁

Sequence Alignment of 48 kD G1 i-antigen
and 55 kD G5 i-antigen nucleotide sequences

```
G1 SEQ ID NO: 1 ATGAAATATAATATTTTATTAAATTTTAATTATTTCTTTATTTATTAATGAATTAAGAGCT
G5 SEQ ID NO: 3 ATGAAAAATAATATTTTAGTAATATTGATTATTTTCATTATTTATCAATTAAATTAATCT
*****|*****

G1 GTTCCATGTCCTGATGGTACTTAGACTCA---AGCTGGAT---TGACTGATGTAGGTGC
G5 GCTAATTGTCCTGTTGGAAGTGAAGTAAACACAGCCGGATAAGTTGA-TGATCTAGGAAC
* * *****

G1 TGCTGATCTTGGTACTTGTGTTAATTGC-AGACCTAATTTTACTATAATGGTGGTGCTG
G5 TCCT-----GCAAAATTGTGTTAATTGTTAGAAA-AACTTTTATTATAATAATGCTGCTG
* ** * * *****

G1 CTTAAGGAGAAGCTAATGGTAATTAACCTTTTCGACGAAATAATGCTGCTAGAGGTATAT
G5 CTT-----TCGTTCC-----TGGTGCTAG---TACGT
*** * * *****

G1 GTGTACCATG-CCA-AATAAACAGA-GTAGGCTCTGTTACCAA-TGCAGGTG--ACTTAG
G5 GTACACCTTGTCCATAAAAAAAGATGCTGGTGCT-TAACCAATCCACCTGCTACT--G
* * * * *

G1 CTACTTTAGCCACATAATGCAGTACTTAATGTCTACTGGCACTGCACCTTGATGATGGAG
G5 CTAATTTAGTCACATAATGTAACGTTAAATGCCCTGCTGGTACCGCAATTGCAGGTGGAG
*** * * * *

G1 TGACAGATGTTTTTG--ATAGATCAGCCGCATAATGTGTTAAATGCAAACCTAACTTTTA
G5 CAACAGATTATGCAGCAATA-ATCA---CAGAATGTGTTAATTGTAGAATTAAATTTTAA
***** * * * *

G1 CTATAATGGTGGTTCTCCTTAAGGTGAAGCTCCTGGCGTTTAAGTTTGTGCTGCTGGTG
G5 ---TAATGA-----AA---ATGCTCC-----AAATTTTAA-----
***** * * * *

G1 TGCCGCTGCAGGTGTTGCTGCCGTTACTAGTTAATGTGTACCTTGCCAACTAAACAAAA
G5 -----TGCAGGTG-----CTAGTACATGCACAGCTTGTCGGTAAACAGAGT
***** * * * *

G1 CGATTCTCCTGCCACTGCAGGT---GCCTAAGCTAATTTAGCCACATAATGTAGCAATTA
G5 TGGTGGTGCAATTGACTGCTGGTAATGCC---GCTACCATAGTCGCATAATGTAACGTCGC
* * * * * *****
```



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G1 ATGTCCTACTGGCACTGTACTTGATGATGGAGTGACACTTGT TTTTAATACATCAGCCAC
G5 ATGTCCTACTGGTACTGCACCTTGATGATGGAGTAACTACTGATTATGTTAGATCATTAC
***** ** * * * * *

G1 ATTATGTGTTAAATGCAGACCTAACTTTTACTATAATGGT-----GGTT---CTCCTTA
G5 AGAATGTGTTAAATGTAGACTTAACTTTTACTATAATGGTAATAATGGTAATACTCCTTT
* ***** ** *

G1 -----AGGTGAA-----GCTCCTGGCGTTTA
G5 CAATCCAGGTAAAGTTAATGCACACCTTGTCGGCAATTAAACCTGCTAATGTTGCTTA
***** ** *

G1 AG-----TTT-----TTGC-----TGCTGG
G5 AGCTACTTTAGGTAATGATGCTACAATAACCGCATAATGTAACGTTGCTAGCCCTGATGG
** *** **** ** *

G1 TGCT-----GCCGCTGCAG-----GTGTTGC-----
G5 TACTATAAGTGCTGCTGGAGTAAATAATTGGGTAGCACAAAACACTGAATGTACTAATTG
* ** * * * * *

G1 -----TGCCGTTACTAGTTAATGTGT
G5 TGCTCCTAACTTTTACAATAATAATGCTCCTAATTTCAATCCAGGTAATAGTACATGCCT
* * * * *

G1 ACCTTGCCAAATAAAACAAAACGATTCTCCTG---CCACTGCAGGTGCCAAGCTAATTT
G5 ACCTTGCCAGCAATAAAGATTATGGTGCTGAAGCCACTGCAGGTGGTGCCGCTACTTT
***** * * * * *

G1 AGCCACATAATGCAGTACTTAATGTCCAACCTGGCACTGCAATT-CAAGACGGAGTGACAC
G5 AGCCAAATAATGTAATATTGCATGCCCTGATGGTACTGCAATTGCTAGT-GGAGCAAC--
***** * * * * *

G1 TTGTTTTAGTAAT-TCATCCACATAATGTTCTTAAT-GCATTGCTAATTACTTTTTTAA
G5 -TAATTAT-GTAATATTATAACAGAAATGT-CTAAATTGTGCTGCTAACTTTTATTTTGA
* * * * *

G1 TGGTAAT---TTCGAAGCAGGTAAAAGTTAATGTTTAAAG--TGTCCAGTAAGTAAACT
G5 TGGTAATAATTTCTAGGCAGGAAGTAGTAGATGC--AAAGCATGTCCAGCAATAAAGTT
***** * * * * *

G1 A-----CTCCAGCACATGCTCCAGGTAATACTGCTACTTAAAGCCACATAATGT----TT
G5 TAAGGCGCTGTAGCAA---CTGCAGGTGGTACTGCTACTTTAATTGCATAATGTGCCCTT
** ***** *

G1 GACCACATGTCCTGCTGGTACAGTACTTGATGATGGAACATCAACTAATTTGTAGCTTC
G5 GA----ATGCCCTGCTGGTACTGTACTCACCGATGGAACAACATCTACTTATAAATAAGC
** * * * * *

G1 CGCAACTGAATGTACTAAATGTTCTGCTGGCTTTTTTGCAATCAAAAACAACTGGTTTTAC
G5 AGCATCTGAATGTGTTAAATGTGCTGCCAACTTTTATACTACAAAATAAAGTATGGGT
* * * * *

G1 AGCAGGTACTGATACATGTACTGAATGTACTAAAAAATTAACCTTCTGGTGCCACAGCTAA
G5 AGCAGGTATTGATACATGTACTAGTTGTAATAAAAAATTAACCTTCTGGCGCTGAAGCTAA
***** * * * * *

G1 AGTATATGCTGAAGCTACTCAAAAAG---TATAATGCGCCTCCACTACTTTTCGCTAAATT
G5 TTTAC---CTGAATCTGCTAAAAAATATATAATGTG-----ATTTCGCTAATTT
* * * * *

G1 TTTATCGATTTCTTATTATTATTCTTTCTATTATTG
G5 TTTATCAATTTCTTATTATTGATTCTTATTATTATTA

Fig. 3b₂

REPLACEMENT SHEET

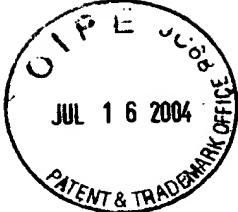
8/27



55 KD i-antigen protein

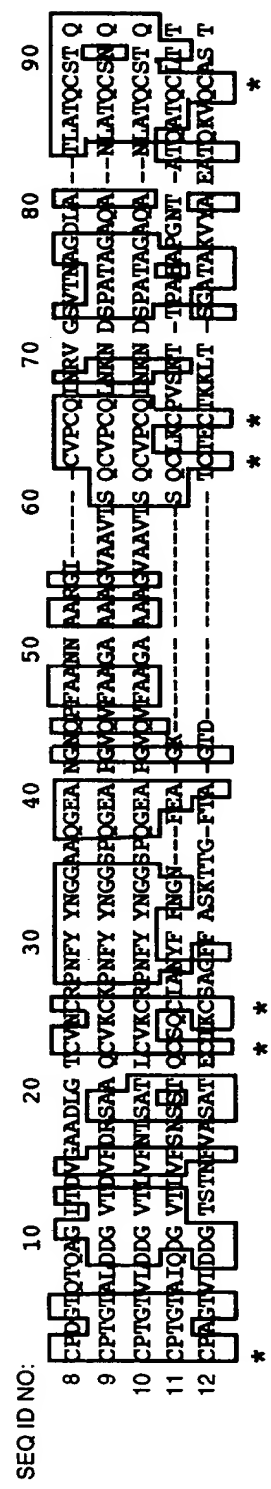
SEQ ID NO: 7	10	20	30	40	50	60
	MKNNILVILI	ISLFINQIKS	ANCPVGTETN	TAGQVDDLGT	PANCVNCQKN	FYYNNAAAFV
	70	80	90	100	110	120
	PGASTCTPCP	QKKDAGAQP	PPATANLVTQ	CNVKCPAGTA	IAGGATDYAA	IITECVNCRI
	130	140	150	160	170	180
	NFYNENAPNF	NAGASTCTAC	PVNRVGGALT	AGNAATIVAQ	CNVACPTGTA	LDDGVTTDYV
	190	200	210	220	230	240
	RSFTECVKCR	LNIFYNGNNG	NTPFNP GKSQ	CTPCPAIKPA	NVAQATLGND	ATITAQC NVA
	250	260	270	280	290	300
	CPDGTISAAG	VNNWVAQNTE	CTNCAPNFYN	NNAPNFNPGN	STCLPCPANK	DYGAEATAGG
	310	320	330	340	350	360
	AATLAKQCNI	ACPDGTAIAS	GATNYVILQT	ECLNCAANFY	FDGNNFQAGS	SRCKACPANK
	370	380	390	400	410	420
	VQGAVATAGG	TATLIAQCAL	ECPAGTVLTD	GTTSTYKQAA	SECVKCAANF	YTTKQTDWVA
	430	440	450	460	470	480
	GIDTCTSCNK	KLTSGAEANL	PESAKKNIQC	DFANFLSISL	LLISYLL**

Fig. 4

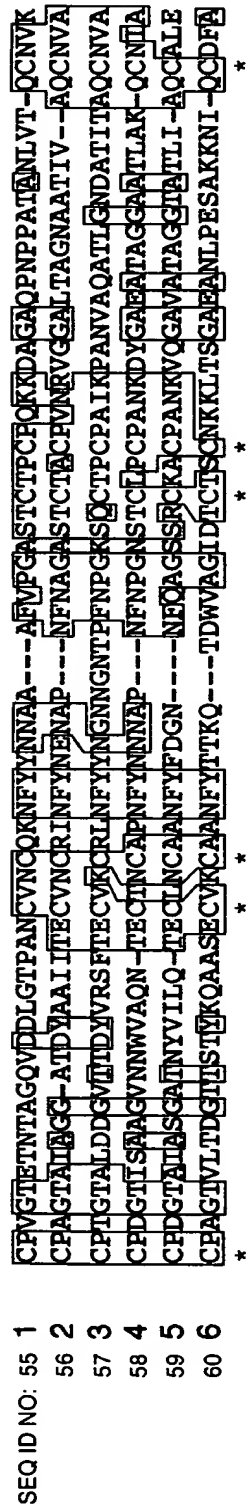


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48 kDa G1 i-antigen repeats



55 kDa G5 i-antigen repeats



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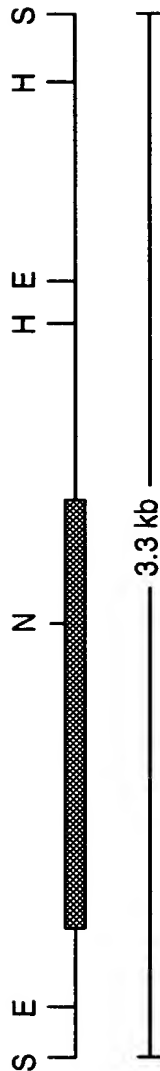


Fig. 6

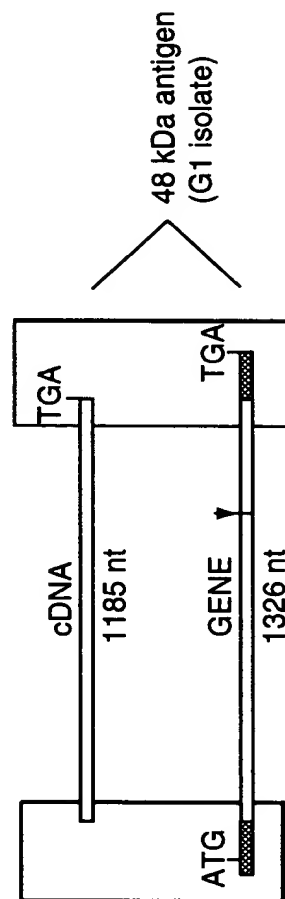


Fig. 7a

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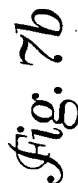
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Fig. 7c



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SEQ ID NO: 61 i-ag
SEQ ID NO: 62 vspA6-S1
20 AVFCDGDTQAG-LTDVGAADLGTVCNCRPNFYNGGAAGQ---EANGNP-FAANNAAR--GICVP---CQINRVGSVTNAGDLATL
61 AVICDQ---GSAGYTDSDSVDAKECKCKCNAPCTACAGTADCKCDANGAAPYLKTNPSDPTGICVSAVIDCG-SAGYTT---DDSVSD
* * * * *
* * * * *
* * * * *
* * * * *

i-ag
vspA6-S1
ATQSTQCPGTGALTDDGVTVDRSAACVCKCPN-----FYNGGSPQ-GE-----APGVQVFAAGAAAGVAAVTSQCVFCOLKNDSPA
AKECK-RCLEGOKPNTAGTQCFSCSDANCCERCDONDVCARCSTGAPPENKCPAATPGCHSSCDGCTENAMTNQADNCKGCKEGHYLKPE
* * * * *
* * * * *
* * * * *

i-ag
vspA6-S1
TAGAQANLATQCSNCPGTGTVLDDGVTVLVTNTSATLCPVCRPNFYNGGSPQGEAPGVQVFAAGAAAGVAAVTSQCVFCOLKNDSPAT
SAAGQSGTCLT-AEBCSTDTTH---FTKKGAGDSKGMCLFCS-----DATHGIAGCKR--CAL---KTLGGEAESTVVCESC-TDKWLTPS-
* * * * *
* * * * *
* * * * *

i-ag
vspA6-S1
AGAQANLATQCSQCPGTGTALQDGVTVLVSNSSTQCSQCLANTFFNGNFEAGKSQCLCPVSKTTPAHAPGNATATQCLTTPP--AGT
-G---N---HCLDNCFAGTYPND-NNLCTSCHDT-CRCC-----NGN--ADRAQCTAC-----YPGVSLLYGSGCTAGTCVKECTGAFGA
* * * * *
* * * * *
* * * * *

i-ag
vspA6-S1
VLDDGTSTNFWASATECTNCSAGFP-----ASKTTGFT-----AGTD-TCTECTTKLTSGATAKVY--AEATQKVQCHSTTPAK 428
NCADGQCTADVGGAKYCAQCKEDGYAPIDGICTAVAAAGRTNVCTAADGTCTKCAGEYT-LMSGGCGYGVAKLPCKSVCTLASNGK 459
* * * * *
* * * * *
* * * * *

Fig. 8

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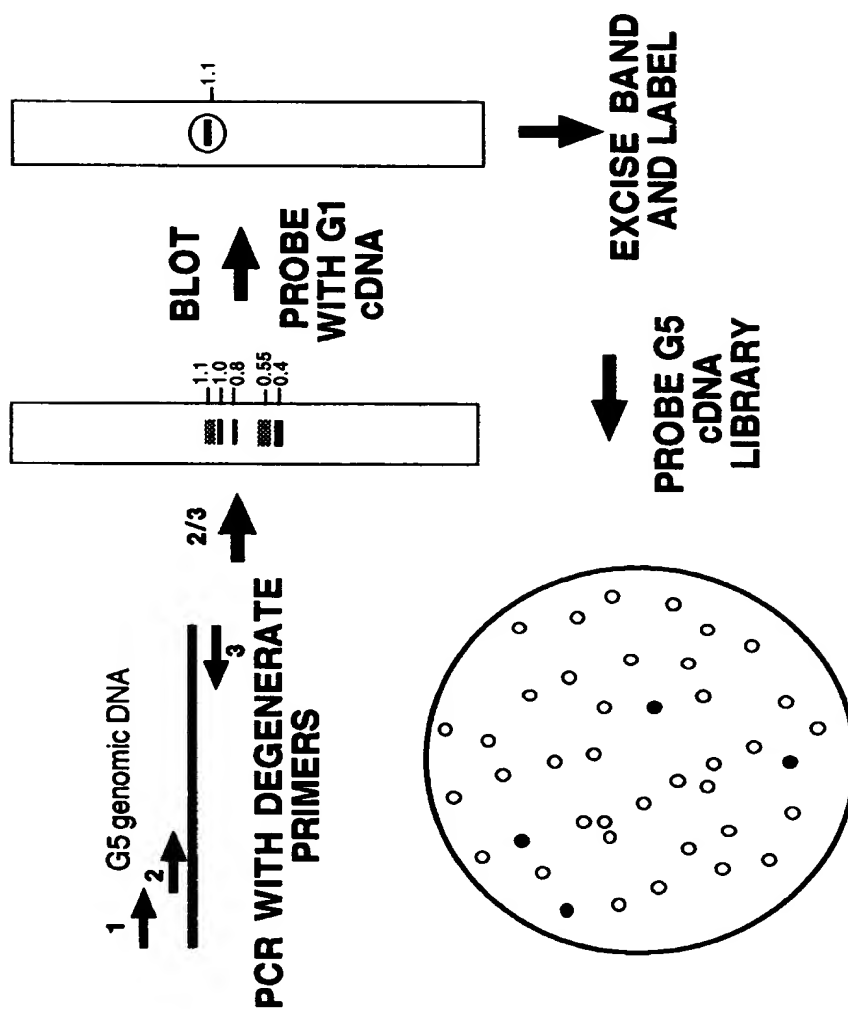


Fig. 9

REPLACEMENT SHEET

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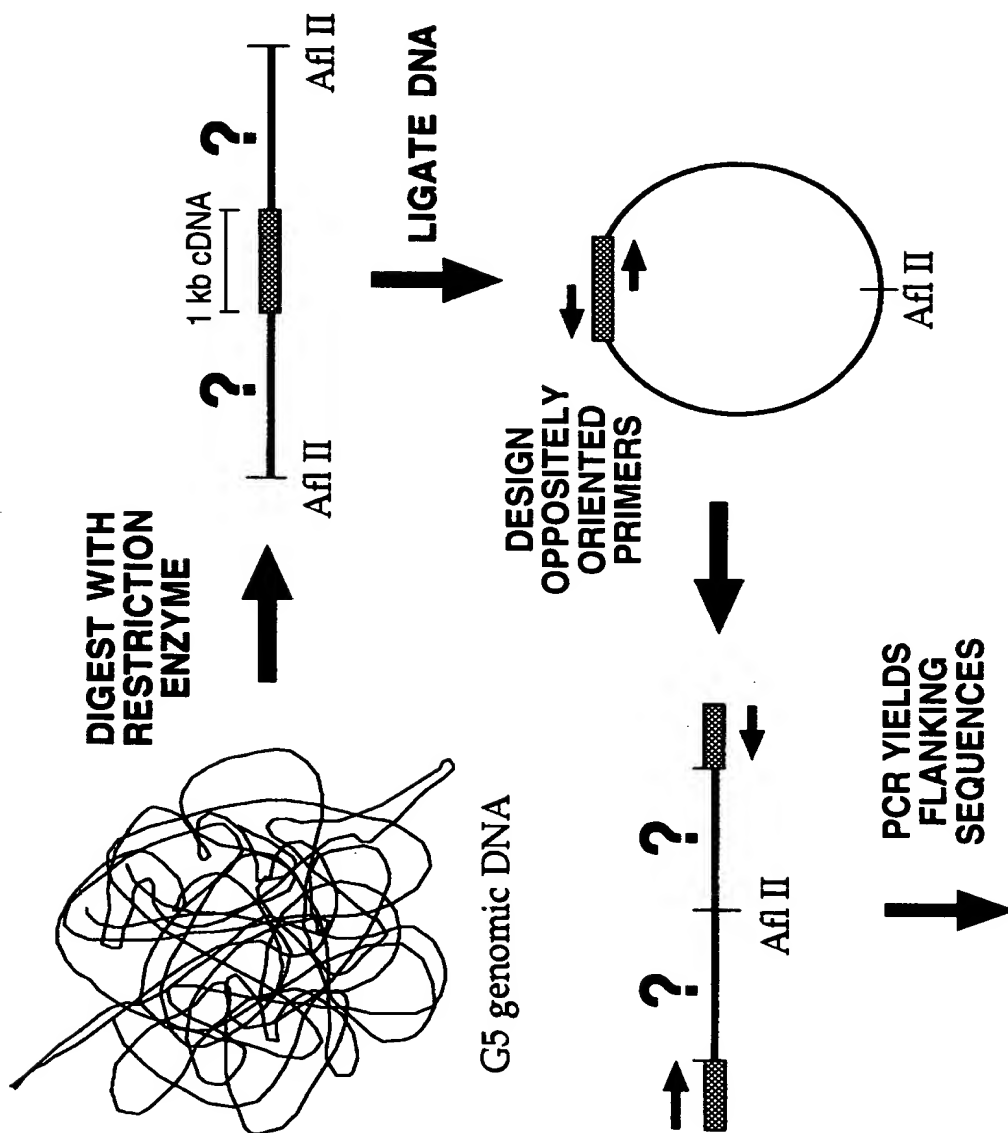


Fig. 10

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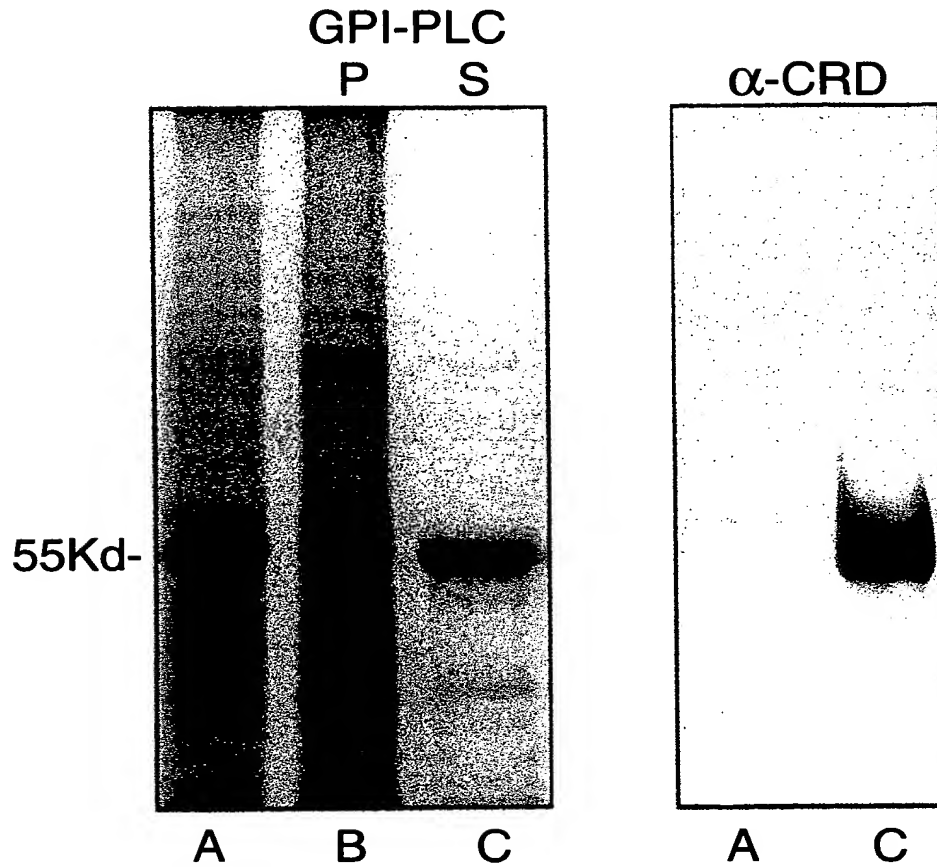


Fig. 11

REPLACEMENT SHEET

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SEQ ID NO: Primers for synthesis of G5 synthetic gene.

- 70 3201:
ATG GGA ATT CAA ATG AAG AAC AAC ATC CTG GTG ATC CTG ATC ATC TCT CTG TTC ATC AAC CAG ATC AAG
TCT GCT AAC TGT OCT GTG GGA ACC GAG ACC AAC ACC GCT GGA CAG GTG
- 71 3202:
CTC CAG GCA CGA AAG CAG CAG CGT TGT TGT AGT AGA AGT TCT TCT GAC AGT TCA CAC AGT TAG CAG GGG
TTC CCA GGT CGT CCA CCT GTC CAG CGG TGT TGG TC
- 72 3203:
CGC TGC TGC TTT CGT GCC TGG AGC TTC TAC CTG TAC CCC TTG TCC TCA GAA GAA GGA CGC TGG AGC TCA
GCC TAA CCC TCC TGC TAC CGC TAA CCT GGT G
- 73 3204:
GAT GAT AGC AGC GTA GTC GGT AGC TCC AGC GAT AGC GGT TCC AGC AGG ACA CTT CAC GTT ACA CTG
GGT CAC CAG GTT AGC GGT AGC AGG AG
- 74 3205:
GCT ACC GAC TAC GCT GCT ATC ATC ACC GAG TGT GTG AAC TGT CGC ATC AAC TTC TAC AAC GAG AAC GCT
CCT AAC TTC AAC GCT GGA GCT TCT ACC TGT ACC GCT TGT OCT GTG AAC CGC GTG GGA GGA GCT CTG ACC
- 75 3206:
GGT GAA AGA GCG CAC GTA GTC GGT GGT CAC TCC GTC GTC CAG AGC GGT TCC GGT AGG ACA AGC CAC GTT
ACA CTG AGC CAC GAT GGT AGC AGC GTT TCC AGC GGT CAG AGC TCC TCC CAC GCG
- 76 3207:
GAC TAC GTG CGC TCT TTC ACC GAG TGT GTG AAG TGT CGC CTG AAC TTC TAC TAC AAC GGA AAC AAC GGA
AAC ACC CCT TTC AAC CCT GGA AAG TCT CAG
- 77 3208:
GTG ATG GTA GCG TCG TTT CCC AGG GTA GCC TGA GCC ACG TTA GCA GGC TTG ATA GCA GGA CAA GGG GTA
CAC TGA GAC TTT CCA GGG TTG AAA GG
- 78 3209:
GGG AAA CGA CGC TAC CAT CAC CGC TCA GTG TAA CGT GGC TTG TCC TGA CGG AAC CAT CTC TGC TGC TGG
AGT GAA CAA CTG GGT GGC TCA GAA C
- 79 3210:
CAG ACA GGT AGA GTT TCC AGG GTT GAA GTT AGG AGC GTT GTT GTT GTA GAA GTT AGG AGC ACA GTT GGT
ACA CTC GGT GTT CTG AGC CAC CCA GTT GTT C
- 80 3211:
CCC TGG AAA CTC TAC CTG TCT GGC TTG TCC TGC TAA CAA GGA CTA CGG AGC TGA GGC TAC CGC TGG AGG
AGC TGC TAC OCT GGC TAA GC
- 81 3212:
GGT CTG CAG GAT CAC GTA GTT GGT AGC TCC AGA AGC GAT AGC GGT TCC GTC AGG ACA AGC GAT GTT ACA
CTG CTT AGC CAG GGT AGC AGC
- 82 3213:
CAA CTA CGT GAT CCT GCA GAC CGA GTG TCT GAA CTG TGC TGC TAA CTT CTA CTT CGA CGG AAA CAA CTT
CCA GGC TGG ATC TTC TCG CTG TAA GG
- 83 3214:
GAG CGA TCA GGG TAG CGG TTC CTC CAG CGG TAG CCA CAG CTC CCT GCA OCT TGT TAG CAG GAC AAG CCT
TAC AGC GAG AAG ATC CAG CCT GG
- 84 3215:
GAA CCG CTA CCC TGA TCG CTC AGT GTG CTC TGG AGT GTC CTG CTG GAA CCG TGC TGA CCG ACG GAA CCA
CCT CTA CCT ACA AGC AGG CTG CTT C
- 85 3216:
GGT GTC GAT TCC AGC CAC CCA GTC GGT CTG CTT GGT GGT GTA GAA GTT AGC AGC ACA CTT CAC ACA CTC
AGA AGC AGC CTG CTT GTA GGT AG
- 86 3217:
GGG TGG CTG GAA TCG ACA OCT GTA CCT CTT GTA ACA AGA AGC TGA OCT CTG GAG CTG AGG CTA ACC TGC
CTG AGT CTG CTA AGA AGA ACA TC
- 87 3218:
GAG GGA TCC TTA TTA CAG CAG GTA AGA GAT CAG CAG CAG AGA GAT AGA CAG GAA GTT AGC GAA GTC
ACA CTG GAT GTT CTT CTT AGC AGA CT

Fig. 12

REPLACEMENT SHEET

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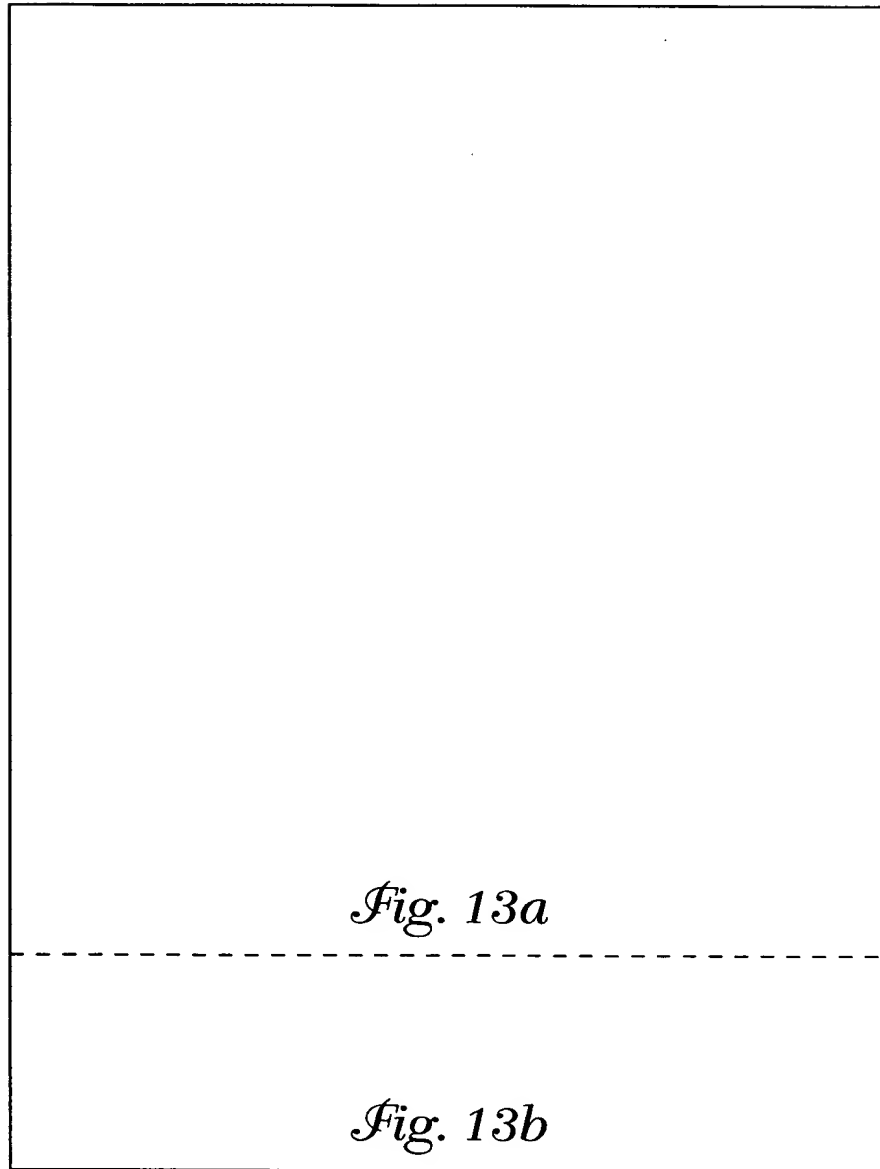


Fig. 13



G5 proline mutant 18/27

SEQ ID NO: 53

10	20	30	40	50	60
ATGAAGAACA	ACATCCCGGT	GATCCTGATC	ATCTCTCTGT	TCATCAACCA	GATCAAGTCT
70	80	90	100	110	120
GCTAACTGTC	CTGTGGGAAC	CGAGACCAAC	ACCGCTGGAC	AGGTGGACGA	CCTGGGAACC
130	140	150	160	170	180
CCTGCTAACT	GTGTGAAGTG	TCAGAAGAAC	TTCTACTACA	ACAACGCTGC	TGCTTTTCGTG
190	200	210	220	230	240
CCTGGAGCTT	CTACCTGTAC	CCCTTGTCCT	CAGAAGAAGG	ACGCTGGAGC	TCAGCCTAAC
250	260	270	280	290	300
CCTCCTGCTA	CCGCTAACCT	GGTGACCCAG	TGTAACGTGA	AGTGTCTCTGC	TGGAACCGCT
310	320	330	340	350	360
ATCGCTGGAG	GAGCTACCGA	CTACGCTGCT	ATCATCACCG	AGTGTGTGAA	CTGTGCGCATC
370	380	390	400	410	420
AACTTCTACA	ACGAGAACGC	TCCTAACTTC	AACGCTGGAG	CTTCTACCTG	TACCGCTTGT
430	440	450	460	470	480
CCTGTGAACC	GTGTGGGAGG	AGCTCTGACC	GCTGGAAACG	CTGCTACCAT	CGTGGCTCAG
490	500	510	520	530	540
TGTAACGTGG	CTTGTCTTAC	CGGAACCGCT	CTGGACGACG	GAGTGACCAC	CGACTACGTG
550	560	570	580	590	600
CGCTCTTTCA	CCGAGTGTGT	GAAGTGTGCG	CTGAACCTCT	ACTACAACGG	AAACAACGGA
610	620	630	640	650	660
AACACCCCTT	TCAACCCCTG	AAAGTCTCAG	TGTACCCCTT	GTCTTGCTAT	CAAGCCTGCT
670	680	690	700	710	720
AACGTGGCTC	AGGCTACCTT	GGGAAACGAC	GCTACCATCA	CCGCTCAGTG	TAACGTGGCT
730	740	750	760	770	780
TGTCCTGACG	GAACCATCTC	TGCTGCTGGA	GTGAACAAC	GGGTGGCTCA	GAACACCGAG
790	800	810	820	830	840
TGTACCAACT	GTGCTCCTAA	CTTCTACAAC	AACAACGCTC	CTAACTTCAA	CCCTGGAAAC
850	860	870	880	890	900
TCTACCTGTC	TGCCTTGTC	TGCTAACAAG	GACTACGGAG	CTGAGGCTAC	CGCTGGAGGA
910	920	930	940	950	960
GCTGCTACCC	TGGCTAAGCA	GTGTAACATC	GCTTGTCTCTG	ACGGAACCGC	TATCGCTTCT
970	980	990	1000	1010	1020
GGAGCTACCA	ACTACGTGAT	CCTGCAGACC	GAGTGTCTGA	ACTGTGCTGC	TAACCTTCTAC
1030	1040	1050	1060	1070	1080
TTCGACGGAA	ACAACTTCCA	GGCTGGATCT	TCTCGCTGTA	AGGCTTGTCC	TGCTAACAAG
1090	1100	1110	1120	1130	1140
GTGCAGGGAG	CTGTGGCTAC	CGCTGGAGGA	ACCGCTACCC	TGATCGCTCA	GTGTGCTCTG
1150	1160	1170	1180	1190	1200
GAGTGTCTTG	CTGGAACCGT	GCTGACCGAC	GGAACCACT	CTACCTACAA	GCAGGCTGCT
1210	1220	1230	1240	1250	1260
TCTGAGTGTG	TGAAGTGTGC	TGCTAACTTC	TACACCACCA	AGCAGACCGA	CTGGGTGGCT

Fig. 13a

REPLACEMENT SHEET

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proline mutant

1270 1280 1290 1300 1310 1320
GGAATCGACA CCTGTACCTC TTGTAACAAG AAGCTGACCT CTGGAGCTGA GGCTAACCTG
1330 1340 1350 1360 1370 1380
CCTGAGTCTG CTAAGAAGAA CATCCAGTGT GACTTCGCTA ACTTCCTGTC TATCTCTCTG
1390 1400 1410 1420 1430 1440
CTGCTGATCT CTTACTACCT GCTG.....

Fig. 13b



20/27

G5 proline mutant protein

	↓	10	20	30	40	50	60
SEQ ID NO: 54		MKNNIPVILI	ISLFINQIKS	ANCPVGTETN	TAGQVDDLGT	PANCVNCQKN	FYYNNAAAFV
		70	80	90	100	110	120
		PGASTCTPCP	QKKDAGAQFN	PPATANLVTQ	CNVKCPAGTA	IAGGATDYAA	IITECVNCRI
		130	140	150	160	170	180
		NFYNENAPNF	NAGASTCTAC	PVNRVGGALT	AGNAATIVAQ	CNVACPTGTA	LDDGVTTDYV
		190	200	210	220	230	240
		RSFTECVKCR	LNFYNGNG	NTPFNPGKSQ	CTPCPAIKPA	NVAQATLGND	ATITAQCINVA
		250	260	270	280	290	300
		CPDGTISAAG	VNNWVAQNT	CTNCAPNFYN	NNAPNFNPGN	STCLPCPANK	DYGAEATAGG
		310	320	330	340	350	360
		AATLAKQCNI	ACPDGTAIAS	GATNYVILQT	ECLNCAANFY	FDGNNFQAGS	SRCKACPANK
		370	380	390	400	410	420
		VQGAVATAGG	TATLIAQCAL	ECPAGTVLTD	GTTSTYKQAA	SECVKCAANF	YTTKQTDWVA
		430	440	450	460	470	480
		GIDTCTSCNK	KLTSGAEANL	PESAKKNIQC	DFANFLSISL	LLISYYLL..

Fig. 14



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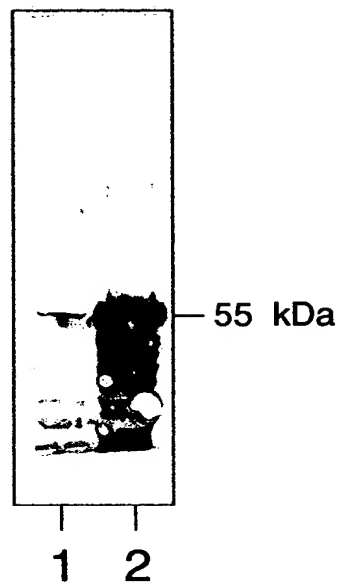


Fig. 15

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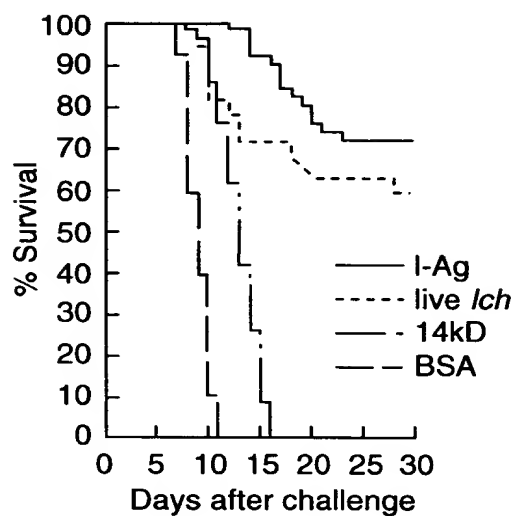


Fig. 16

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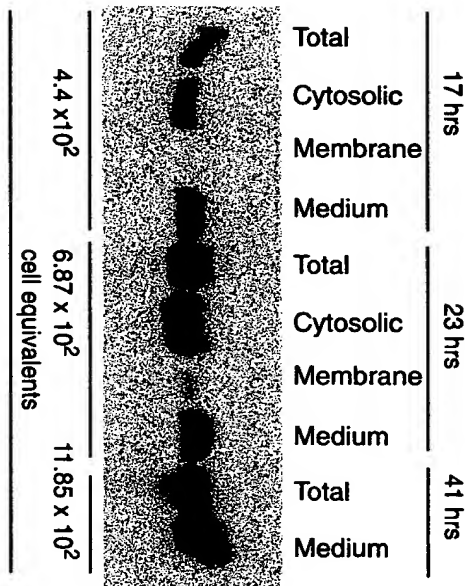


Fig. 17

REPLACEMENT SHEET

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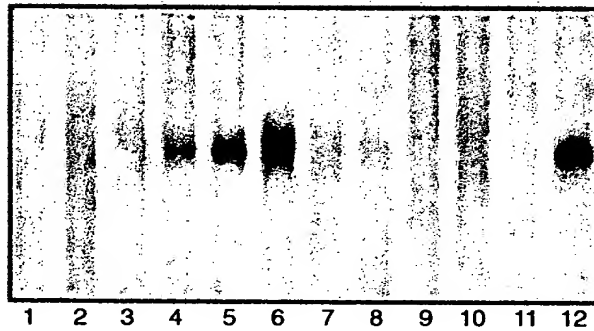


Fig. 18

REPLACEMENT SHEET



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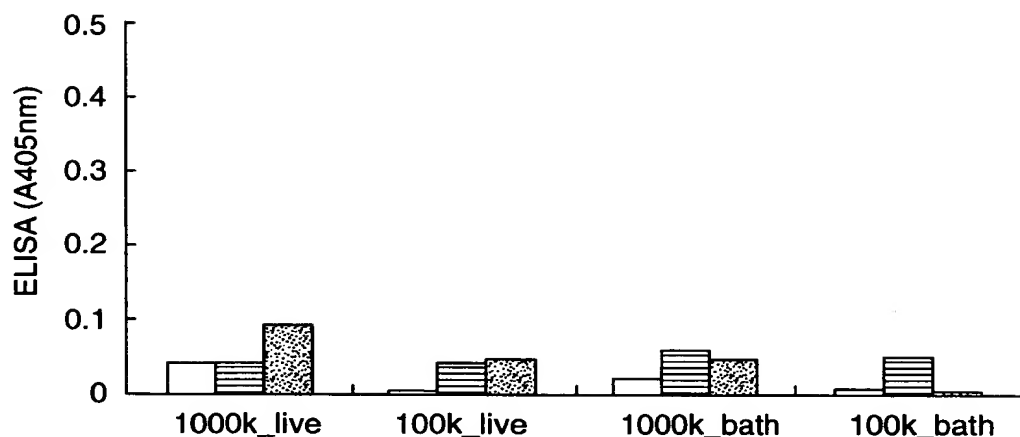


Fig. 19a

□ Week 2
 ▨ Week 4
 ▩ Week 6

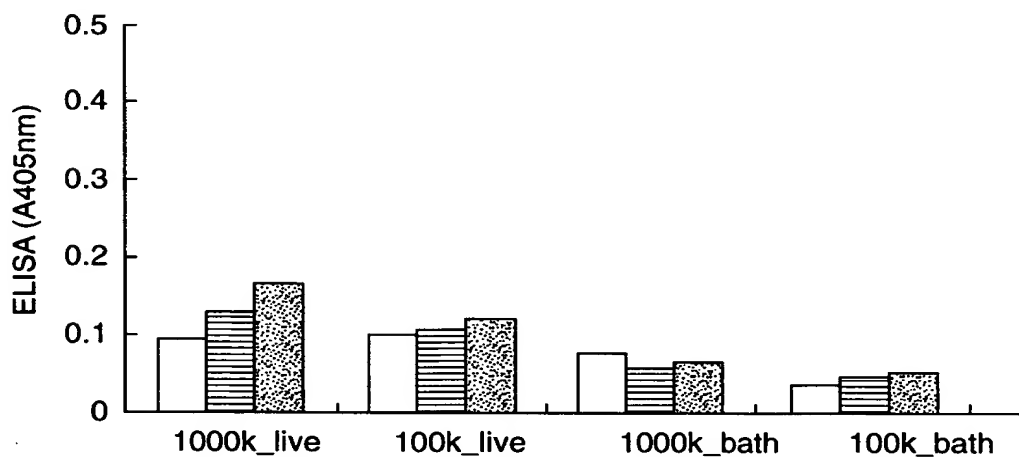
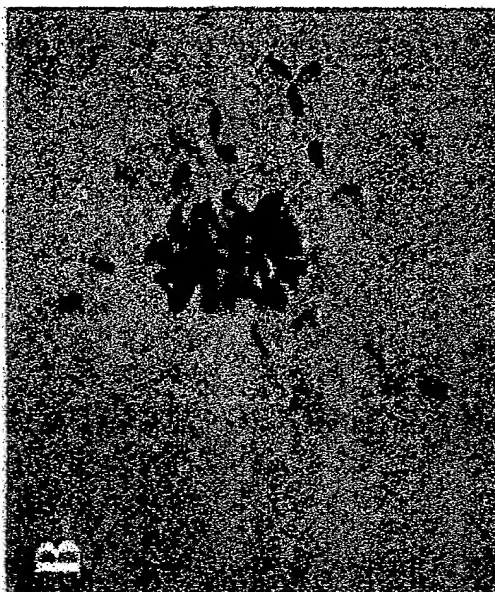


Fig. 19b

□ Week 2
 ▨ Week 4
 ▩ Week 6

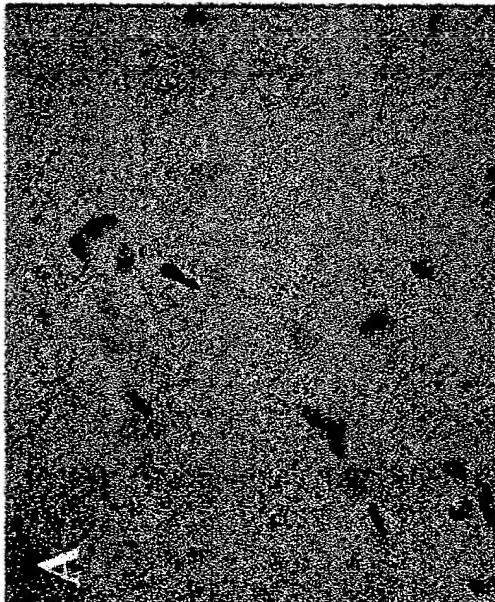
REPLACEMENT SHEET

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Serum: anti-live TG1 (1 : 20)

Fig. 20b



Serum: anti-live Tneo (1 : 20)
(negative control)

Fig. 20a

REPLACEMENT SHEET

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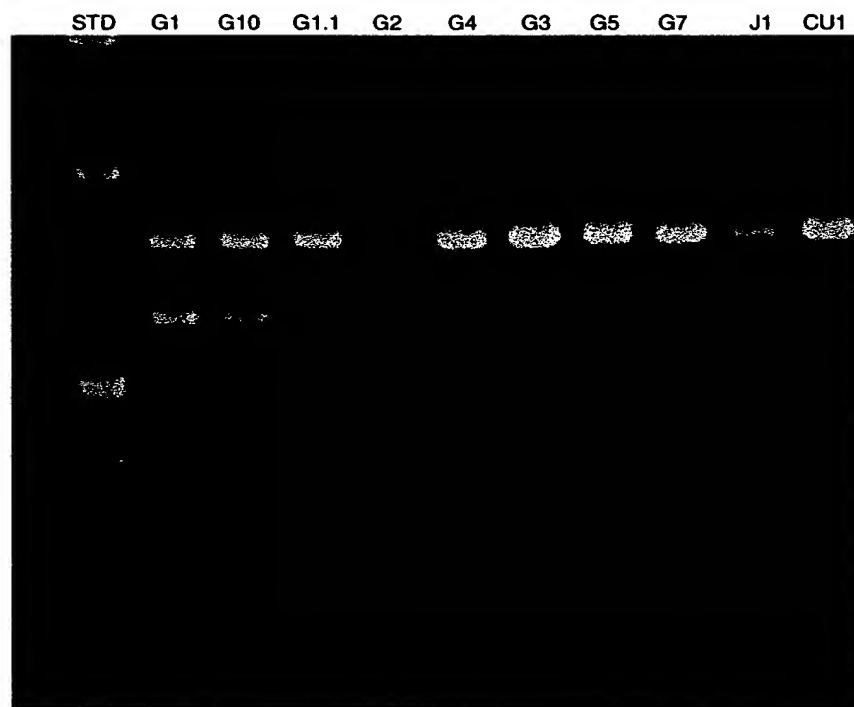


Fig. 21